OIPE

RAW SEQUENCE LISTING   DATE: 10/04/2001
PATENT APPLICATION· US/09/736,960   TIME: 17:50:41

Input Set : A:\-5-1-1.app
Output Set· N:\CRF3\10042001\I736960.raw

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  3  <110· APPLICANT· In, Peter
  4         Garman, Jonathan David
  5         Candia III, Albert Frederick
  6         Arbor Vita Corporation
  8  <120> TITLE OF INVENTION: CLASP-5 Transmembrane Protein    ENTERED
 10  <130· FILE REFERENCE: 020054-000511US
 12  <140· CURRENT APPLICATION NUMBER: US 09/736,960
 13  <141> CURRENT FILING DATE: 2001-09-20
 15  <150· PRIOR APPLICATION NUMBER· US 60/160,860
 16  <151· PRIOR FILING DATE  1999-10-21
 18  <150· PRIOR APPLICATION NUMBER· US 60/162,498
 19  <151· PRIOR FILING DATE. 1999-10-29
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 22  <151· PRIOR FILING DATE  1999-12-13
 24  <150· PRIOR APPLICATION NUMBER. US 60/176,195
 25  <151· PRIOR FILING DATE: 2000-01-14
 27  <150· PRIOR APPLICATION NUMBER  US 60/182,296
 28  <151· PRIOR FILING DATE: 2000-02-14
 30  <150· PRIOR APPLICATION NUMBER  US 09,547,276
 31  <151· PRIOR FILING DATE  2000-04-11
 33  <150· PRIOR APPLICATION NUMBER  US 60·196,267
 34  <151· PRIOR FILING DATE: 2000-04-11
 36  <150· PRIOR APPLICATION NUMBER: US 60/196,460
 37  <151· PRIOR FILING DATE: 2000-04-11
 39  <150· PRIOR APPLICATION NUMBER  US 60/196,527
 40   151· PRIOR FILING DATE  2000-04-11
 42   150· PRIOR APPLICATION NUMBER: US 60/196,528
 43   151· PRIOR FILING DATE· 2000-04-11
 45   150· PRIOR APPLICATION NUMBER: US 09/687,837
 46   151· PRIOR FILING DATE  2000-10-13
 48   150· PRIOR APPLICATION NUMBER: US 60 240,503
 49   151· PRIOR FILING DATE  2000-10-13
 51   150· PRIOR APPLICATION NUMBER  US 60 240,508
 52   151· PRIOR FILING DATE  2000-10-13
 54   150· PRIOR APPLICATION NUMBER: US 60 240,539
 55   151· PRIOR FILING DATE  2000-10-13
 57   150· PRIOR APPLICATION NUMBER: US 60 240,543
 58   151· PRIOR FILING DATE  2000-10-13
 60   160· NUMBER OF SEQ ID NOS: 134
 62   170· SOFTWARE: PatentIn Ver. 2.1
 64   210· SEQ ID NO: 1
 65   211· LENGTH: 7215
 66   212· TYPE: DNA
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Input Set : A:\-5-1-1.app
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74 <222> LOCATION: (112)..(6159)
75 <223> OTHER INFORMATION: human CLASP-5
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80 aagcctcagt tttatgacca tgtggagcca gtggactttg aaggacttct g atg aca 117
81                                                         Met Thr
82                                                           1
84 cac ctg aac agc ctg gat gtg cag ctt gcc cag gag ctc ggg gac ttc 165
85 His Leu Asn Ser Leu Asp Val Gln Leu Ala Gln Glu Leu Gly Asp Phe
86          5                  10                  15
88 act gat gac gac ttg gac gtg gtg ttc acg cca aag gaa tgt agg act 213
89 Thr Asp Asp Asp Leu Asp Val Val Phe Thr Pro Lys Glu Cys Arg Thr
90          20                  25                  30
92 ttg cag ccc tct ttg ccg gag gaa ggg gtt gaa ctg gac cct cat gtc 261
93 Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro His Val
94 35                  40                  45                  50
96 agg gac tgt gtt cag acc tac atc cgt gag tgg cta atc gtg aac cgg 309
97 Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val Asn Arg
98                  55                  60                  65
100 aaa aac caa gga agt cca gaa atc tgt ggc ttt aaa aag act gga tct 357
101 Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr Gly Ser
102                  70                  75                  80
104 cga aaa gat ttt cac aag acg ctt ccg aaa cag acg ttt gag tcg gaa 405
105 Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu Ser Glu
106          85                  90                  95
108 acc ttg gag tgc agt gaa ccc gct gct cag gca ggc ccc cgc cac tta 453
109 Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg His Leu
110          100                 105                 110
112 aac gtg ctg tgc gac gtg tct ggg aaa ggc ccc gtc act gcc tgt gac 501
113 Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala Cys Asp
114 115                 120                 125                 130
116 ttt gac ctc cgc agc ctg cag cct gac aag cgg cta gaa aac ctc ctg 549
117 Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn Leu Leu
118                 135                 140                 145
120 cag caa gtg agt gcc gag gac ttt gag aag cag aac gag gag gcc cgg 597
121 Gln Gln Val Ser Ala Glu Asp Phe Glu Lys Gln Asn Glu Glu Ala Arg
122                 150                 155                 160
124 agg acc aac agg cag gcc gag ctc ttt gcc ctt tac cca tca gtg gac 645
125 Arg Thr Asn Arg Gln Ala Glu Leu Phe Ala Leu Tyr Pro Ser Val Asp
126          165                 170                 175
128 gag gag gat gct gtg gaa ata cgt cca gta cca gaa tgt ccc aag gaa 693
129 Glu Glu Asp Ala Val Glu Ile Arg Pro Val Pro Glu Cys Pro Lys Glu
130          180                 185                 190
132 cac ctg ggc aac aga ata ttg gtc aag ttg ctg acc ttg aag ttc gag 741
133 His Leu Gly Asn Arg Ile Leu Val Lys Leu Leu Thr Leu Lys Phe Glu
134 195                 200                 205                 210
136 att gaa att gag ccc ctg ttt gcc agc att gcc ctc tac aat att gag 789
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Input Set : A:\ 5 1 1.app
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138                215                220                225
140 gaa agg aaa aag atc tca gaa aat ttt cac tgt gac ctg aac tct gac   837
141 Glu Arg Lys Lys Ile Ser Glu Asn Phe His Cys Asp Leu Asn Ser Asp
142            230                235                240
144 cag ttc aaa gga ttt ctg cga gct cac acg cct tca gtg gcc gca tca   885
145 Gln Phe Lys Gly Phe Leu Arg Ala His Thr Pro Ser Val Ala Ala Ser
146            245                250                255
148 agt cag gcg aga tct gca gtc ttc tca gtc acc tac ccg tcc tca gac   933
149 Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser Ser Asp
150      260                265                270
152 atc tac ctg gta gtc aag att gaa aaa gtc ctg cag cag gga gat att   981
153 Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly Asp Ile
154 275                280                285                290
156 gga gac tgt gca gag ccc tac acg gtt atc aaa gaa agt gat ggt gga  1029
157 Gly Asp Cys Ala Glu Pro Tyr Thr Val Ile Lys Glu Ser Asp Gly Gly
158            295                300                305
160 aag agt aaa gaa aag att gaa aaa cta aaa ctc caa gct gaa tcc ttc  1077
161 Lys Ser Lys Glu Lys Ile Glu Lys Leu Lys Leu Gln Ala Glu Ser Phe
162            310                315                320
164 tgc cag cgt ttg ggg aaa tac cgg atg ccc ttt gcc tgg gca ccc ata  1125
165 Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp Ala Pro Ile
166            325                330                335
168 agc tta tca agc ttc ttc aat gtc tcc acc ctt gag agg gag gta act  1173
169 Ser Leu Ser Ser Phe Phe Asn Val Ser Thr Leu Glu Arg Glu Val Thr
170      340                345                350
172 gat gtg gac tct gtg gtt ggg aga agc cca gtg ggt gaa cgg agg aca  1221
173 Asp Val Asp Ser Val Val Gly Arg Ser Pro Val Gly Glu Arg Arg Thr
174 355                360                365                370
176 ttg gcc caa tct aga agg ctt tct gaa aga gcc ctc tcc ttg gag gaa  1269
177 Leu Ala Gln Ser Arg Arg Leu Ser Glu Arg Ala Leu Ser Leu Glu Glu
178            375                380                385
180 aat ggg gtt gga tcc aac ttc aaa acc tcc act ctg agc gtt agc agc  1317
181 Asn Gly Val Gly Ser Asn Phe Lys Thr Ser Thr Leu Ser Val Ser Ser
182            390                395                400
184 ttt ttc aag cag gaa gga gat cgc ctt agc gat gaa gac tta ttc aag  1365
185 Phe Phe Lys Gln Glu Gly Asp Arg Leu Ser Asp Glu Asp Leu Phe Lys
186            405                410                415
188 ttt tta gct gac tac aaa aga tca tca tcc tta cag aga cga gtc aag   14 3
189 Phe Leu Ala Asp Tyr Lys Arg Ser Ser Ser Leu Gln Arg Arg Val Lys
190      420                425                430
192 tca att cca ggc ttg cta aga ctg gag att tct aca gct cca gag atc  1461
193 Ser Ile Pro Gly Leu Leu Arg Leu Glu Ile Ser Thr Ala Pro Glu Ile
194 435                440                445                450
196 atc aat tgc tgt ctg act cct gaa atg ctg ccc gtg aaa ccc ttt cct  1509
197 Ile Asn Cys Cys Leu Thr Pro Glu Met Leu Pro Val Lys Pro Phe Pro
198            455                460                465
200 gaa aac cgg aca cgc ccg cac aaa gag att ttg gaa ttt cca aca cga  1557
201 Glu Asn Arg Thr Arg Pro His Lys Glu Ile Leu Glu Phe Pro Thr Arg
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RAW SEQUENCE LISTING   DATE: 10/04/2001
PATENT APPLICATION: US/09/736,960   TIME: 17:50:41

Input Set : A:\-5-1-1.app
Output Set: N:\CRF3\10042001\I736960.raw

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204 gaa gta tat gtc cct cac act gtg tac aga aac ctt ctc tat gtc tac   1605
205 Glu Val Tyr Val Pro His Thr Val Tyr Arg Asn Leu Leu Tyr Val Tyr
206     485                 490                 495
208 cca cag agg ctg aac ttt gta aac aaa cta gca tca gcc cgg aac att   1653
209 Pro Gln Arg Leu Asn Phe Val Asn Lys Leu Ala Ser Ala Arg Asn Ile
211     500                 505                 510
212 aca ata aag atc cag ttt atg tgt gga gaa gat gct agc aat gcg atg   1701
213 Thr Ile Lys Ile Gln Phe Met Cys Gly Glu Asp Ala Ser Asn Ala Met
214 515                 520                 525                 530
216 ccg gtc atc ttt gga aaa tcc agc ggg cct gaa ttt ctg cag gaa gtg   1749
217 Pro Val Ile Phe Gly Lys Ser Ser Gly Pro Glu Phe Leu Gln Glu Val
218             535                 540                 545
220 tac aca gct gtt aca tac cat aat aag tct cct gac ttt tat gaa gaa   1797
221 Tyr Thr Ala Val Thr Tyr His Asn Lys Ser Pro Asp Phe Tyr Glu Glu
222         550                 555                 560
224 gtg aaa att aag ctc ccc gct aag ctc aca gta aat cac cac ctc ctg   1845
225 Val Lys Ile Lys Leu Pro Ala Lys Leu Thr Val Asn His His Leu Leu
226     565                 570                 575
228 ttc acc ttc tac cat atc agc tgt cag cag aag caa gga gcc tcc gtg   1893
229 Phe Thr Phe Tyr His Ile Ser Cys Gln Gln Lys Gln Gly Ala Ser Val
230     580                 585                 590
232 gaa act ctc ctg gga tat tca tgg ctg cca att ctc tta aat gaa cgt   1941
233 Glu Thr Leu Leu Gly Tyr Ser Trp Leu Pro Ile Leu Leu Asn Glu Arg
234 595                 600                 605                 610
236 ctt caa act gga tcc tac tgt ctc cca gtt gcc ttg gaa aaa ttg cca   1989
237 Leu Gln Thr Gly Ser Tyr Cys Leu Pro Val Ala Leu Glu Lys Leu Pro
238             615                 620                 625
240 ccc aac tac tcc atg cat tct gct gag aaa gtc cca tta cag aat cct   2037
241 Pro Asn Tyr Ser Met His Ser Ala Glu Lys Val Pro Leu Gln Asn Pro
242         630                 635                 640
244 ccc att aag tgg gct gaa gga cat aag gga gta ttt aat att gaa gtg   2085
245 Pro Ile Lys Trp Ala Glu Gly His Lys Gly Val Phe Asn Ile Glu Val
246         645                 650                 655
248 caa gct gtt tct tct gta cac acc cag gac aac cac ctg gag aag ttc   2133
249 Gln Ala Val Ser Ser Val His Thr Gln Asp Asn His Leu Glu Lys Phe
250     660                 665                 670
252 ttc acc ctc tgc cac tcc ctg gag agc cag gtg acc ttc ccc atc cgc   2181
253 Phe Thr Leu Cys His Ser Leu Glu Ser Gln Val Thr Phe Pro Ile Arg
254 675                 680                 685                 690
256 gtg ctg gat cag aaa atc agc gag atg gcg ctg gag cat gag ctg aag   2229
257 Val Leu Asp Gln Lys Ile Ser Glu Met Ala Leu Glu His Glu Leu Lys
258             695                 700                 705
260 ctc agc atc atc tgc ctg aac tcc tcc cgc ctg gag ccg ctc gtg ctc   2277
261 Leu Ser Ile Ile Cys Leu Asn Ser Ser Arg Leu Glu Pro Leu Val Leu
262             710                 715                 720
264 ttc ctc cac ctg gtg ctg gac aag ctc ttc cag ctg tcc gtg cag ccc   2325
265 Phe Leu His Leu Val Leu Asp Lys Leu Phe Gln Leu Ser Val Gln Pro
266         725                 730                 735
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Input Set : A:\-5-1-1.app
Output Set: N:\CRF3\10042001\I736960.raw

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269 Met Val Ile Ala Gly Gln Thr Ala Asn Phe Ser Gln Phe Ala Phe Glu
270     740               745               750
272 tcc gtg gtg gcc atc gcc aac agt ctg cac aac agc aag gac ctg agc    2421
273 Ser Val Val Ala Ile Ala Asn Ser Leu His Asn Ser Lys Asp Leu Ser
274 755           760               765               770
276 aag gac cag cat ggg agg aac tgc ctg ctg gct tcc tac gtg cac tac    2469
277 Lys Asp Gln His Gly Arg Asn Cys Leu Leu Ala Ser Tyr Val His Tyr
278               775               780               785
280 gtc ttc cgc ctg cca gag gtg caa agg gat gtg ccc aag tca ggc gct    2517
281 Val Phe Arg Leu Pro Glu Val Gln Arg Asp Val Pro Lys Ser Gly Ala
282               790               795               800
284 ccc act gcc ctc cta gac cct cgg agc tac cac acg tat ggc cgc aca    2565
285 Pro Thr Ala Leu Leu Asp Pro Arg Ser Tyr His Thr Tyr Gly Arg Thr
286           805               810               815
288 tca gct gct gct gtg agt tca aag ctg ctg cag gcc cgg gtg atg agc    2613
289 Ser Ala Ala Ala Val Ser Ser Lys Leu Leu Gln Ala Arg Val Met Ser
290     820               825               830
292 agc agt aac cca gac ctc gcg ggg aca cac tcc gca gca gac gag gaa    2661
293 Ser Ser Asn Pro Asp Leu Ala Gly Thr His Ser Ala Ala Asp Glu Glu
294 835               840               845               850
296 gtg aag aac atc atg tct tca aag atc gcc gat cgc aac tgc agc cga    2709
297 Val Lys Asn Ile Met Ser Ser Lys Ile Ala Asp Arg Asn Cys Ser Arg
298               855               860               865
300 atg tct tac tat tgc tct ggc agt agt gat gct cca agt tca cct gca    2757
301 Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser Pro Ala
302               870               875               880
304 gcc cca agg cca gcc agc aaa aag cat ttc cat gag gag ctt gcc ctt    2805
305 Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu Ala Leu
306           885               890               895
308 cag atg gtg gtc agc acc gga atg gtg aaa agc atg gcc cag cac gta    2853
309 Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln His Val
310     900               905               910
312 cat aac atg gac aaa cgg gac agt ttt cgg agg act cgt ttt tct gac    2901
313 His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe Ser Asp
314 915               920               925               930
316 cgt ttc atg gat gac ata act act att gtt aat gtg gtc acc tcg gaa    2949
317 Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr Ser Glu
318               935               940               945
320 att gca gcc ctt tta gta aaa cca cag aag gaa aat gaa cag gcg gaa    2997
321 Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln Ala Glu
322               950               955               960
324 aag atg aac atc agc ctg gct ttc ttc ttg tat gac ctt ctc tcc ctc    3045
325 Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu Ser Leu
326     965               970               975
328 atg gat cgg ggc ttt gtg ttt aac ctc atc aga cat tat tgc agc cag    3093
329 Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys Ser Gln
330     980               985               990
332 ctg tca gcc aag ctc agt gac ctt cca acg ctc att tcc gtt gga cta    3141
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VERIFICATION SUMMARY

DATE: 10/04/2001

PATENT APPLICATION: US/09/736,960

TIME: 17:50:42

Input Set : A:\-5-1-1.app
Output Set: N:\CRF3\10042001\I736960.raw

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1271 M 336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:1275 M 336 w: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L 1279 M 336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L 4113 M 341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
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L 4174 M 341 W  (46) "n" or "Xaa" used, for SEQ ID# 61
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L:4229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
L:4230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
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L:4237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
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L:8140 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (95) SEQUENCE:
L:8146 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (96) SEQUENCE:
L:8152 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (97) SEQUENCE:
L:8158 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (98) SEQUENCE:
L:8164 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (99) SEQUENCE:
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Input Set : A:\-5-1-1.app
Output Set: **N:\CRF3\10042001\I736960.raw**

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L:8176 M 300 W· (50) Intentionally skipped Sequence, : Sequence Id (101) SEQUENCE·
L:8182 M.300 W (50) Intentionally skipped Sequence, : Sequence Id (102) SEQUENCE·
L 8188 M 300 W (50) Intentionally skipped Sequence, · Sequence Id (103) SEQUENCE·
L 8194 M 300 W. (50) Intentionally skipped Sequence, · Sequence Id (104) SEQUENCE
L 8200 M:300 W. (50) Intentionally skipped Sequence, : Sequence Id (105) SEQUENCE:
L 8206 M·300 W· (50) Intentionally skipped Sequence, : Sequence Id (106) SEQUENCE:
L:8212 M:300 W. (50) Intentionally skipped Sequence, Sequence Id (107) SEQUENCE:
L:8218 M 300 W (50) Intentionally skipped Sequence, : Sequence Id (108) SEQUENCE·
L 8224 M:300 W (50) Intentionally skipped Sequence, . Sequence Id (109) SEQUENCE.
L 8230 M 300 W: (50) Intentionally skipped Sequence, · Sequence Id (110) SEQUENCE:
L:8236 M 300 W. (50) Intentionally skipped Sequence, : Sequence Id (111) SEQUENCE:
L 8242 M:300 W. (50) Intentionally skipped Sequence, : Sequence Id (112) SEQUENCE:
L 8248 M:300 W. (50) Intentionally skipped Sequence, · Sequence Id (113) SEQUENCE:
L 8254 M:300 W. (50) Intentionally skipped Sequence, Sequence Id (114) SEQUENCE:
L 8260 M 300 W (50) Intentionally skipped Sequence, Sequence Id (115) SEQUENCE:
L 8266 M 300 W (50) Intentionally skipped Sequence, Sequence Id (116) SEQUENCE:
L:8272 M·300 W· (50) Intentionally skipped Sequence, : Sequence Id (117) SEQUENCE:
L 8313 M 341 W. (46) "n" or "Xaa" used, for SEQ ID#:118
L:8369 M:341 W. (46) "n" or "Xaa" used, for SEQ ID#:119